Appl. No. 10/656,482
Amdt. dated March 23, 2007
Reply to Office Action of September 27, 2006

PATENT

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

Claims 1-45 (canceled).

Claim 46 (currently amended): A method of producing a genomic library enriched for genes and regulatory sequences from [[a]] an eukaryotic genome, said method comprising:

cleaving [[a]] an eukaryotic genome into fragments of double stranded DNA;

denaturing the double stranded DNA fragments;

selectively hybridizing the fragments at Cot values of between approximately 0.01 and 100 to yield a population of double-stranded, repetitive DNA fragments and a single-stranded population of non-repetitive fragments enriched for genes;

separating the two populations by hydroxyapatite chromatography;

selecting the non-repetitive population single-stranded population of non-repetitive fragments enriched for genes; and,

inserting the non-repetitive population of fragments single-stranded population of non-repetitive fragments enriched for genes into a vector to produce a genomic library enriched for genes and regulatory sequences from [[a]] an eukaryotic genome.

Claim 47 (currently amended): [[A]] The method of claim 46 that further comprises the step of sequencing the fragments enriched for genes.

Claim 48 (currently amended): The method of claim 46 wherein the step of cleaving comprises randomly shearing the genomic DNA eukaryotic genome to yield fragments.

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Claim 49 (previously presented): The method of claim 46 wherein the step of cleaving is by methylation insensitive restriction enzymes.

Claim 50 (currently amended): The method of claim 46 further comprising the step of size fractionating said ~~genomic DNA~~ fragments before inserting the fragments into a vector.

Claim 51 (previously presented): The method of claim 50 wherein the fractionated DNA fragments range from about 0.5 to about 4 kilobase pairs.

Claim 52 (previously presented): The method of claim 46 wherein the vector is selected from a group consisting of phage and plasmid.

Claim 53 (previously presented): The method of claim 52 wherein the phage vector is M13.

Claim 54 (previously presented): The method of claim 46 wherein said genome is a plant genome.

Claim 55 (currently amended): The method of claim 54 wherein said plant genome is selected from the group consisting of: ~~maize, rice, Brassica, soybean, and wheat~~ maize genome, rice genome, Brassica genome, soybean genome, and wheat genome.

Claim 56 (previously presented): The method of claim 46 wherein said genome is a cereal genome.

Claim 57 (currently amended): The method of claim 46 wherein said genome is a mammalian genome.